

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 18, 2002, 05:11:43 ; Search time 116.57 Seconds
(Without alignments)
390.303 Million cell updates/sec

Title: US-09-719-748-2_COPY_13_275

Perfect score: 1343
Sequence: 1 YDIGEELSGGFAIVKCKRE.....LVKTRKRLTIGELALHPWI 263

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: SP_TREMBL_19:*
2: SP_Archea:*
3: SP_Bacteria:*
4: SP_Fungi:*
5: SP_Human:*
6: SP_Invertebrate:*
7: SP_Mhc:*
8: SP_Organelle:*
9: SP_Phage:*
10: SP_Plant:*
11: SP_Protist:*
12: SP_Virus:*
13: SP_Vertebrate:*
14: SP_Unclassified:*
15: SP_Virus:*
16: SP_Bacteriophage:*
17: SP_Archea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1332	99.2	370	4	075892
2	1321	98.4	370	4	0901K4
3	1297	96.6	370	11	090YU4
4	1128	84.0	1430	11	090YU4
5	1125	83.8	345	11	090YU4
6	1124	83.7	367	4	090YU4
7	1121	83.5	454	4	043293
8	1106	82.4	448	11	054784
9	1106	82.4	448	11	088764
10	1073	79.9	303	11	088861
11	745.5	55.5	1435	5	044997
12	660.5	49.2	2762	5	P91255
13	646.5	48.1	641	6	090B69
14	642.5	47.8	992	4	090C05
15	636.5	47.4	907	13	090850
16	636	47.4	371	11	091X58

17	634	47.2	372	11	0923E7	0923E7 mus musculus
18	631.5	47.0	611	11	091X59	091X59 cavia porcea
19	627.5	46.7	1721	5	0961U1	0961U1 drosophila
20	627.5	46.7	7107	5	090V47	090V47 drosophila
21	617.5	46.0	6658	5	076281	076281 drosophila
22	607.5	45.2	451	5	016980	016980 aplysia cal
23	599.5	44.6	795	4	0966V1	0966V1 homo sapien
24	577.5	43.0	1211	5	023260	023260 caenorhabdi
25	576.5	42.9	446	5	0955K9	0955K9 drosophila
26	575	42.8	925	5	001651	001651 drosophila
27	574	42.7	577	5	096V81	096V81 drosophila
28	574	42.7	732	5	096V71	096V71 drosophila
29	574	42.7	786	5	096V79	096V79 drosophila
30	574	42.7	832	5	001653	001653 drosophila
31	574	42.7	913	5	090V76	090V76 drosophila
32	574	42.7	1289	4	090V25	090V25 homo sapien
33	573	42.7	2959	11	090JF1	090JF1 rattus norv
34	569.5	42.4	596	4	090H83	090H83 homo sapien
35	566	42.1	569	5	001652	001652 drosophila
36	562.5	41.9	6831	5	023550	023550 caenorhabdi
37	562.5	41.9	7160	5	023551	023551 caenorhabdi
38	557.5	41.5	335	5	061269	061269 mytilus gal
39	557.5	41.5	878	5	096V22	096V22 mytilus gal
40	541	40.3	4650	4	015598	015598 homo sapien
41	541	40.3	26926	4	010466	010466 homo sapien
42	538	40.1	775	6	097754	097754 trypanosoma
43	537	40.0	623	5	096V80	096V80 drosophila
44	525	39.1	638	5	090VX9	090VX9 drosophila
45	521	38.8	980	10	0910R4	0910R4 arabidopsis

ALIGNMENTS

RESULT 1
ID 075892 PRELIMINARY; PRT; 370 AA.
AC 075892;
DT 01-NOV-1998 (TREMBL) 08, Created
DT 01-NOV-1998 (TREMBL) 08, Last sequence update
DT 01-DEC-2001 (TREMBL) 19, Last annotation update
DE DAP-KINASE RELATED PROTEIN 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RX MEDLINE=20094983; PubMed=10629061;
RA Ithal B., Shanl G., Cohen O., Kissel J.L., Kimchi A.;
RT "Death-associated protein kinase-related protein 1, a novel
Serine/Threonine kinase involved in apoptosis.";
RL Mol. Cell. Biol. 20:1044-1054(2000).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AF052941; AAC35001.1; -
DR HSP: Q63450; 1A06
DR InterPro: IPR000719; Euk_Pkinase.
DR InterPro: IPR002290; Ser_thr_Pkinase.
DR Pfam: PF00069; Pkinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_DGM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 370 AA; 42923 MW; 09502B4ADC20F91 CRC64;

Query Match 99.2% Score 1332; DB 4; Length 370;
Best Local Similarity 99.6% Pred. No. 1.5e-95;
Matches 262; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
1 YDIGEELSGGFAIVKCKREKSTGLEVAKFKKRSRSHRGVSRERIEVSLRQVL 60

Db 23 YDIGEELSGGFAIVKCKREKSTGLEVAKFKIKKQSRASRGVSRREIEREVSILRQVL 82
QY 61 HHNVITLHDVYENRTDVVHIIELVSGGELFDPLAOKESLSEBEATSFKQILDGVNYLHT 120
Db 83 HHNVITLHDVYENRTDVVHIIELVSGGELFDPLAOKESLSEBEATSFKQILDGVNYLHT 142
QY 121 KKAIAFDLKPENIMLDKNIPPHIKLIDFGLAHEIEDGVFEKNIFGTPPEVAPETVNYE 180
Db 143 KKAIAFDLKPENIMLDKNIPPHIKLIDFGLAHEIEDGVFEKNIFGTPPEVAPETVNYE 202
QY 161 PLGLEADWMSIGVITYILLSGASPLGDTKQETLANITSVSYDDEFFSHTSELADFT 240
Db 203 PLGLEADWMSIGVITYILLSGASPLGDTKQETLANITSVSYDDEFFSHTSELADFT 262
QY 241 RKLIVKETRRKRLTIOEALRHPWI 263
Db 263 RKLIVKETRRKRLTIOEALRHPWI 285

RESULT 2
Q9UIK4 PRELIMINARY; PRT; 370 AA.
ID Q9UIK4
AC Q9UIK4; 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE DEATH-ASSOCIATED PROTEIN KINASE 2.
GN DAPK2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99303018; PubMed=10376525;
RA Kawai T., Nomura F., Hoshino K., Copeland N.G., Gilbert D.J.,
RA Jenkins N.A., Akira S.;
RT Death-associated protein kinase 2 is a new calcium/calmodulin-
RT dependent protein kinase that signals apoptosis through its catalytic
RT activity.*;
RL Oncogene 18:3471-3480(1999).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AB018001; BAA8064.1; .
DR HSSP: Q63450; 1A06.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase.1
DR PRINTS: PR00109; TYRKINASE.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 370 AA; 42898 MW; 035E914BBD881A2 CRC64;

Query Match 98.4%; Score 1321; DB 4; Length 370;
Best Local Similarity 98.9%; Pred. No. 1,1e-94;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YDIGEELSGGFAIVKCKREKSTGLEVAKFKIKKQSRASRGVSRREIEREVSILRQVL 60
Db 23 YDIGEELSGGFAIVKCKREKSTGLEVAKFKIKKQSRASRGVSRREIEREVSILRQVL 82
QY 61 HHNVITLHDVYENRTDVVHIIELVSGGELFDPLAOKESLSEBEATSFKQILDGVNYLHT 120
Db 83 HHNVITLHDVYENRTDVVHIIELVSGGELFDPLAOKESLSEBEATSFKQILDGVNYLHT 142
QY 121 KKAIAFDLKPENIMLDKNIPPHIKLIDFGLAHEIEDGVFEKNIFGTPPEVAPETVNYE 180
Db 143 KKAIAFDLKPENIMLDKNIPPHIKLIDFGLAHEIEDGVFEKNIFGTPPEVAPETVNYE 202

QY 181 PLGLEADWMSIGVITYILLSGASPLGDTKQETLANITSVSYDDEFFSHTSELADFT 240
Db 203 PLGLEADWMSIGVITYILLSGASPLGDTKQETLANITSVSYDDEFFSHTSELADFT 262
QY 241 RKLIVKETRRKRLTIOEALRHPWI 263
Db 263 RKLIVKETRRKRLTIOEALRHPWI 285

RESULT 3
Q9QYM4 PRELIMINARY; PRT; 370 AA.
ID Q9QYM4
AC Q9QYM4; 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE DEATH-ASSOCIATED PROTEIN KINASE 2.
GN DAPK2 OR DAPK2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99303018; PubMed=10376525;
RA Kawai T., Nomura F., Hoshino K., Copeland N.G., Gilbert D.J.,
RA Jenkins N.A., Akira S.;
RT Death-associated protein kinase 2 is a new calcium/calmodulin-
RT dependent protein kinase that signals apoptosis through its catalytic
RT activity.*;
RL Oncogene 18:3471-3480(1999).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AB018002; BAA8064.1; .
DR HSSP: Q63450; 1A06.
DR MGD: MGI1341297; DapK2.
DR InterPro: IPR000719; DapK2.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; pkinase.1
DR PRINTS: PR00109; TYRKINASE.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 370 AA; 42769 MW; 7DA6E29C4DE615B3 CRC64;

Query Match 96.6%; Score 1297; DB 11; Length 370;
Best Local Similarity 97.3%; Pred. No. 7.7e-93;
Matches 256; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 YDIGEELSGGFAIVKCKREKSTGLEVAKFKIKKQSRASRGVSRREIEREVSILRQVL 60
Db 23 YDIGEELSGGFAIVKCKREKSTGLEVAKFKIKKQSRASRGVSRREIEREVSILRQVL 82
QY 61 HHNVITLHDVYENRTDVVHIIELVSGGELFDPLAOKESLSEBEATSFKQILDGVNYLHT 120
Db 83 HHNVITLHDVYENRTDVVHIIELVSGGELFDPLAOKESLSEBEATSFKQILDGVNYLHT 142
QY 121 KKAIAFDLKPENIMLDKNIPPHIKLIDFGLAHEIEDGVFEKNIFGTPPEVAPETVNYE 180
Db 143 KKAIAFDLKPENIMLDKNIPPHIKLIDFGLAHEIEDGVFEKNIFGTPPEVAPETVNYE 202
QY 181 PLGLEADWMSIGVITYILLSGASPLGDTKQETLANITSVSYDDEFFSHTSELADFT 240
Db 203 PLGLEADWMSIGVITYILLSGASPLGDTKQETLANITSVSYDDEFFSHTSELADFT 262
QY 241 RKLIVKETRRKRLTIOEALRHPWI 263
Db 263 RKLIVKETRRKRLTIOEALRHPWI 285

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RESULT 4
ID 09JUP7 PRELIMINARY: PRT: 1430 AA.
AC 09JUP7;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE DEATH ASSOCIATED PROTEIN KINASE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA Klmchl A.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: X97048; CAA65762.1; -.
DR HSSP: Q63450.1A06.
DR InterPro: IPR002110; ANK.
DR InterPro: IPR000488; Death.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; ank. 8.
DR Pfam: PF00069; pkinase. 1.
DR SMART: SM00248; ANK. 8.
DR SMART: SM00005; DEATH. 1.
DR SMART: SM00220; S_TKC. 1.
DR PROSITE: PS50088; ANK_REPEAT. 7.
DR PROSITE: PS50297; ANK_REPEAT_REGION. 1.
DR PROSITE: PS50017; DEATH_DOMAIN. 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP. 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM. 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST. 1.
DR ANK repeat; ATP-binding; Kinase; Repeat.
KM Serine/threonine-protein kinase; Transferrase.
SQ SEQUENCE 1430 AA; 159843 MW; 81C8356CD14BBE8 CRC64;

Query Match 84.0%; Score 1128; DB 11; Length 1430;
Best Local Similarity 80.2%; Pred. No. 6e-79;
Matches 211; Conservative 37; Mismatches 15; Indels 0; Gaps 0;

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DE 2310039H24RIK PROTEIN (FRAGMENT).
GN 2310039H24RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CS7BL/6J; TISSUE=TONGUE;
RX MEDLINE=21085660; Pubmed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aizawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamakura I.,
RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nkaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baidarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK009701; BAB26448.1; -.
DR HSSP: Q63450.1A06.
DR MCD: MGI:1916885; 2310039H24RIK.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; pkinase. 1.
DR PRINTS: PR00109; TYRKINASE.
DR SMART: SM00220; S_TKC. 1.
DR SMART: SM00219; TYRK. 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP. 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM. 1.
DR ATP-binding; Transferrase.
KW NON TER 345 345
SQ SEQUENCE 345 AA; 39776 MW; FF7D1B4F71CA39C0 CRC64;

Query Match 83.8%; Score 1125; DB 11; Length 345;
Best Local Similarity 79.8%; Pred. No. 1.6e-79;
Matches 210; Conservative 38; Mismatches 15; Indels 0; Gaps 0;

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09BTL8
ID 09BTL8 PRELIMINARY: PRT: 367 AA.
AC 09BTL8;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE SIMILAR TO DEATH-ASSOCIATED PROTEIN KINASE 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=MELANOMA.;
RC Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: BC003614; AA03614.1; -
DR HSSP: 063450; 1A06.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; pkinase.1.
DR PRINTS: PR00109; TYRKINASE.
DR SMART: SM00220; S_TKc; 1.
DR SMART: SM00219; tyrc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KM ATP-binding; kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 367 AA; 42115 MW; 42EDIDE7191FE3FD CRC64;

Query Match 83.7%; Score 1124; DB 4; Length 367;
Best Local Similarity 79.5%; Pred. No. 2.1e-79;
Matches 209; Conservative 41; Mismatches 13; Indels 0; Gaps 0;
QY 1 YDIGELSGGQPAIVKCKREKSTGLEVAKFKKRSRRGVSREIEREVNLTROVL 60
DB 13 YDIGELSGGQPAIVKCKREKSTGLEVAKFKKRSRRGVSREIEREVNLTROVL 72
QY 1 HNNVITLHDVYENKRDVYVHILEVSGGELFDEFLAKESLSEEARSTFKQILDGVNYLHT 120
DB 61 HNNVITLHDVYENKRDVYVHILEVSGGELFDEFLAKESLSEEARSTFKQILDGVNYLHT 120
QY 73 HNNVITLHDVYENKRDVYVHILEVSGGELFDEFLAKESLSEEARSTFKQILDGVNYLHT 132
DB 121 KRIAFDLPENIMLDNIPRIPIKILDFGLAHIEDGVEKNFTGPEFAPEIYVNE 180
QY 133 LQIAHFDLPENIMLDNIPRIPIKILDFGLAHIEDGVEKNFTGPEFAPEIYVNE 192
DB 133 LQIAHFDLPENIMLDNIPRIPIKILDFGLAHIEDGVEKNFTGPEFAPEIYVNE 192
QY 181 PLGLEADMSIGVITYILLSGASPLGDTKQETLANITSVSYDPEEFPSHTSELAKDFI 240
DB 193 PLGLEADMSIGVITYILLSGASPLGDTKQETLANITSVSYDPEEFPSHTSELAKDFI 252
QY 241 RRLVKEKTRKRLTIOEALRHPMI 263
DB 253 RRLVKEKTRKRLTIOEALRHPMI 275
RESULT 7
ID 043293 PRELIMINARY: PRT: 454 AA.
AC 043293;
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 18, Last annotation update)
DE ZIP-KINASE.
GN ZIPK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE=98147805; PubMed=9488481;
RA Kawai T., Matsumoto M., Takeda K., Sanjo H., Akira S.;
RT "ZIP kinase, a novel serine/threonine kinase which mediates
RT apoptosis.";
RT Mol. Cell. Biol. 18:1642-1651(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=9923879; PubMed=10356987;
RA Murata-Hori M., Suizu F., Iwasaki T., Kikuchi A., Hosoya H.;
RT "ZIP kinase identified as a novel myosin regulatory light chain kinase
RT in HeLa cells.";
RL FEBS Lett. 451:81-84(1999).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AB007144; BAA24955.1; -
DR EMBL: AB022341; BAA81746.1; -
DR HSSP: 063450; 1A06.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase.1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KM ATP-binding; kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 454 AA; 52535 MW; 56773008A6A61CFO CRC64;

Query Match 83.5%; Score 1121; DB 4; Length 454;
Best Local Similarity 79.8%; Pred. No. 4.7e-79;
Matches 210; Conservative 36; Mismatches 17; Indels 0; Gaps 0;
QY 1 YDIGELSGGQPAIVKCKREKSTGLEVAKFKKRSRRGVSREIEREVNLTROVL 60
DB 13 YDIGELSGGQPAIVKCKREKSTGLEVAKFKKRSRRGVSREIEREVNLTROVL 72
QY 61 HNNVITLHDVYENKRDVYVHILEVSGGELFDEFLAKESLSEEARSTFKQILDGVNYLHT 120
DB 73 HNNVITLHDVYENKRDVYVHILEVSGGELFDEFLAKESLSEEARSTFKQILDGVNYLHT 132
QY 121 KRIAFDLPENIMLDNIPRIPIKILDFGLAHIEDGVEKNFTGPEFAPEIYVNE 180
DB 133 KRIAFDLPENIMLDNIPRIPIKILDFGLAHIEDGVEKNFTGPEFAPEIYVNE 192
QY 181 PLGLEADMSIGVITYILLSGASPLGDTKQETLANITSVSYDPEEFPSHTSELAKDFI 240
DB 193 PLGLEADMSIGVITYILLSGASPLGDTKQETLANITSVSYDPEEFPSHTSELAKDFI 252
QY 241 RRLVKEKTRKRLTIOEALRHPMI 263
DB 253 RRLVKEKTRKRLTIOEALRHPMI 275
RESULT 8
ID 054784 PRELIMINARY: PRT: 448 AA.
AC 054784;
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE ZIP-KINASE.
GN ZIPK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98147805; PubMed=9488481;
RA Kawai T., Matsumoto M., Takeda K., Sanjo H., Akira S.;
RT "ZIP kinase, a novel serine/threonine kinase which mediates
RT apoptosis.";
RT Mol. Cell. Biol. 18:1642-1651(1998).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

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166 FGTFEVAPELVNYPELGLEADMWSICVITYILSGASPFPGDTKQETLANITSVSYDFD 227
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Db      121  FGTPEFAPEIVNPEPLGLEADMSIGVITYILLSGASPFGLDTPKOETLANITAVSYD 180
QY      226  EEFSSHSTSELAQDFIRKLKLVKTRKRLTIOEALRHPMI 263
Db      181  EEFSSQTSSELAQDFIRKLKLVKTRKRLTIOEALRHPMI 218

RESULT  11
ID      044997  PRELIMINARY; PRT; 1435 AA.
AC      044997;
DT      01-JUN-1998 (TREMBLrel. 06, Created)
DT      01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT      01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE      K12C11.4 PROTEIN.
GN      K12C11.4.
OS      Caenorhabditis elegans.
OC      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC      Rhabditidae; Peloderinae; Caenorhabditis.
OX      NCBI_TaxID=6239;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN-BRISTOL N2;
RX      MEDLINE=99069613; PubMed=9851916;
RA      None;
RT      "Genome sequence of the nematode C. elegans: a platform for
RT      investigating biology. The C. elegans Sequencing Consortium.";
RL      Science 282:2012-2018(1998).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN-BRISTOL N2;
RX      Wansley P., Kramer J.;
RT      "The sequence of C. elegans cosmid K12C11.";
RL      Submitted (JAN-1998) to the EMBL/Genbank/DBJ databases.
RN      [3]
RP      SEQUENCE FROM N.A.
RC      STRAIN-BRISTOL N2;
RX      Waterston R.;
RT      Submitted (MAR-2001) to the EMBL/Genbank/DBJ databases.
CC      -1- SIMILARITY: BELONGS TO THE EMBL/Genbank/DBJ databases.
DR      EMBL; AF043701; AAK19971.1; -.
DR      HSSP; Q63450; 1A06.
DR      InterPro: IPR002110; ANK.
DR      InterPro: IPR000488; ANK.
DR      InterPro: IPR002190; Ser_thr_pkinase.
DR      InterPro: IPR002290; Ser_thr_pkinase.
DR      Pfam; PF00023; ank; 7.
DR      Pfam; PF00531; death; 1.
DR      SMART; SM00248; ANK; 7.
DR      SMART; SM00005; DEATH; 1.
DR      SMART; SM00220; S_TKC; 1.
DR      PROSITE; PS50086; ANK_REPEAT; 7.
DR      PROSITE; PS50297; ANK_REPEAT; 7.
DR      PROSITE; PS50017; DEATH_DOMAIN; 1.
DR      PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR      PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW      ANK repeat; ATP-binding; Repeat; Serine/threonine-protein kinase;
KW      Transferrase
SQ      SEQUENCE 1435 AA; 160602 MW; C73EB605C37FB732 CRC64;

Query Match          55.5%; Score 745.5; DB 5; Length 1435;
Best Local Similarity 56.5%; Pred. No. 3e-49;
Matches 144; Conservative 45; Mismatches 63; Indels 3; Gaps 2;

QY      10  GGFAYVKKCRKSTGLELYAAKFIKRSASRGVSRGVEEIEREVSILROYL-HHNVTYTLH 68
Db      80  GGFAYVVRVRBRKTKGEYAAKFIKRRYATSRGVTQRNEREVRVLOKIRGNSNVVEIH 139
QY      69  DYVNRFDVVHILEVSGGELFDFLOKESLSEEAATSFIKOILDGVNVLTKKIAHFDL 128
Db      140  AVYETADVYIIVLELVSGGELFDFHVCACECLDEVEAAAFIKOILLAVRHLSLHLYHLDI 199

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QY      129  KPENIMLDKNIDPIPHIKLIDFGLAEIDGVEFKNIGFPERVADPEIVNPEPLGLEAD 188
Db      200  KPEVMVL--KQSDSQIKIIDFGLSEIEGAVYKDMVGTPPEFAPEIVNPEALSPATDM 257
QY      189  WSGIVTYIILLSGASPFGLDTPKOETLANITVSYDPEEFSSHSTSELAQDFIRKLKLV 248
Db      258  MAVGVYTYIILLSGASPFGLDNDRETFESNITRVRHYHSDRYFNKTSKHAQDFYLRVHDV 317
QY      249  RKRITIOEALRHPMI 263
Db      318  DQATVEECLQHPMI 332

RESULT  12
ID      P91255  PRELIMINARY; PRT; 2762 AA.
AC      P91255;
DT      01-MAY-1997 (TREMBLrel. 03, Created)
DT      01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT      01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE      HYPOTHETICAL 306.5 KDA PROTEIN.
GN      F12F3.2.
OS      Caenorhabditis elegans.
OC      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC      Rhabditidae; Peloderinae; Caenorhabditis.
OX      NCBI_TaxID=6239;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN-BRISTOL N2;
RX      MEDLINE=99069613; PubMed=9851916;
RA      None;
RT      "Genome sequence of the nematode C. elegans: a platform for
RT      investigating biology. The C. elegans Sequencing Consortium.";
RL      Science 282:2012-2018(1998).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN-BRISTOL N2;
RX      Fulton B., Wohldmann P.;
RT      "The sequence of C. elegans cosmid F12F3.";
RL      Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.
RN      [3]
RP      SEQUENCE FROM N.A.
RC      STRAIN-BRISTOL N2;
RX      Waterston R.;
RT      "Direct Submission.";
RL      Submitted (NOV-2001) to the EMBL/Genbank/DBJ databases.
DR      EMBL; U80022; AAC25886.2; -.
KW      Hypothetical protein.
SQ      SEQUENCE 2762 AA; 306525 MW; C964CCEB0322084 CRC64;

Query Match          49.2%; Score 660.5; DB 5; Length 2762;
Best Local Similarity 47.3%; Pred. No. 2.8e-42;
Matches 125; Conservative 61; Mismatches 69; Indels 9; Gaps 3;

QY      1  YIGBELSGGFAYVKKCRKSTGLELYAAKFIKRSASRGVSRGVEEIEREVSILROYL 60
Db      195  YIIHELKGAGVGYRATKATGKTMANKVQVRP-----GVKKEVYHESMMNQLH 248
QY      61  HNNVTLDHYENRDTDVHILEVSGGELFDFLOKESL-SEEAATSFIKOILDGVNVLH 119
Db      249  HEKLIHLAEAFDGMENMLLEEFVSGGELFDFKILIEDDSLMSSEEEVRDYMHOILLGVS 308
QY      120  TKKIAHFDLKPENIMLDKNIPRPHIKLIDFGLAEIDGVEFKNIGFPERVADPEIVN 179
Db      309  KNOYIHLDLKPENIMLLAKN--SNEKLIIDFGLARKADPKKSVKLLFGTPEFCAPAEV 366
QY      180  EPLGLEADMSIGVITYIILLSGASPFGLDTPKOETLANITVSYDPEEFSSHSTSELAQ 239
Db      367  QPVELSTDMVMVGVISVLLSGLSPEFGSDDEDTLANVASASDMDPDPSPDDVSDLAQ 426
QY      240  IRKLLVETRRKRLTIOEALRHPMI 263

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RESULT 15
ID 098850 PRELIMINARY; PRT; 907 AA.
AC 098850;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE NEURONAL MYOSIN LIGHT CHAIN KINASE 1.
GN GFMCLK1.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Carassius.
OX NCBI_TaxId=7957;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COMMON COMET;
RX MEDLINE=97067382; PubMed=8910795;
RA Jian X., Szabo B.G., Schmidt J.T.;
RT "Myosin light chain kinase: expression in neurons and upregulation
RT during axon regeneration.";
RL J. Neurobiol. 31:379-391(1996).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: U61731; AAB41402.1; -.
DR HSSP: P56276; ITRK
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003598; IG_C2.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR002290; Ser_thr_kinase.
DR Pfam: PF00041; fn3; 1.
DR Pfam: PF00047; Ig; 2.
DR Pfam: PF00069; pkinase; 1.
DR SMART: SM00060; FN3; 1.
DR SMART: SM00408; IGC2; 2.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE: PS00101; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Immunoglobulin domain; Kinase;
DR Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 907 AA; 101423 MW; 3B6BA33BF312362C CRC64;

Query Match 47.4%; Score 636.5; DB 13; Length 907;
Best Local Similarity 45.8%; Pred. No. 4.8e-41;
Matches 121; Conservative 56; Mismatches 78; Indels 9; Gaps 3;

QY 1 YDIGELSGGQFAIVKCKREKSTGLEVAKFTKKRQSRASRGVSRRELEREVSILROYL 60
DB 470 YDVERRLTGKGAVFKLEIKSTKVMAGKFTKAYSAR-----BKDNVROEIAIMNDLR 523
QY 61 HHNVITLDHYENRTDVVHILEIVSGELDFLAQK-SLSPEEATSFIKOILDGCVNYLH 119
DB 524 HPKLVOQVDAREGKTDIVMVEWMSGELFERIIDEDELTEREYIKYIMLDIVDGVSTIH 583
QY 120 TKKIHPELKPENIMLDKKNIPPIKILIDGLAHEIDEGVEKNIFGTPEFAPEIYNY 179
DB 584 KGGIVHLDLKPENIMCVNKT--GSKIKLIDGLARLENAGSLKVLFGTPEFAPEVINY 641
QY 180 EPLGLEADMSIGVITYTLLSGASPELGDTKOETLANITSVYDPEDEFESHTELADF 239
DB 642 EALSTADMSIGVICYLVLSGLSPFGNDNDNETLSNVTSATWDFEADFDEISDEAKDF 701
QY 240 IRKLIVKETRRRLTIQEALRHPWI 263
DB 702 ISNLLKDKMKARLSGDQCFQHPWL 725
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Page 9

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